WHAT IS CLAIMED IS:

1. A method of generating a set of amino acid sequences representative of at least one polypeptide of interest, the method comprising:

(a) computationally generating a plurality of proteolytic cleavage products from the at least one polypeptide of interest;

(b) computationally analyzing said plurality of proteolytic cleavage products according to at least one parameter defining a characteristic of an amino acid sequence; and

(c) selecting a set of proteolytic cleavage products from said plurality of proteolytic cleavage products according to predetermined criteria for each of said at least at least parameter, thereby generating the set of amino acid sequences representative of the at least one polypeptide of interest.

2. The method of claim 1, wherein said plurality of proteolytic cleavage products are generated according to a proteolytic cleavage pattern of at least one proteolytic agent.

3. The method of claim 2, wherein said at least one proteolytic agent is selected from the group consisting of a proteolytic enzyme and a proteolytic chemical.

4. The method of claim 3, wherein said proteolytic enzyme is selected from the group consisting of trypsin, chymotrypsin, subtilisin, pepsin, V8 protease, thrombin and elastase.

5. The method of claim 3, wherein said proteolytic chemical is selected from the group consisting of cyanogen bromide and 2-nitro-5-thiocyanobenzoate.

6. The method of claim 1, wherein said at least one parameter defining said characteristic of said amino acid sequence is selected from the group consisting of molecular weight, amino acid composition, hydrophobicity, hydrophilicity, charge, secondary structure, heterogeneity, length, post-translational modifications, polarity, solubility, amphipathic nature, sequence and immunogenicity.

7. A computer readable storage media comprising a database of amino acid sequences corresponding to at least one polypeptide of interest, said database of amino acid sequences being generated by:

(a) computationally generating a plurality of proteolytic cleavage products from the at least one polypeptide of interest; and

(b) computationally analyzing said plurality of proteolytic cleavage products according to at least one parameter defining a characteristic of an amino acid sequence; and

(c) storing a sequence of each of said proteolytic cleavage products thereby generating said database of amino acid sequences.

8. The computer readable storage media of claim 7, wherein said plurality of proteolytic cleavage products are generated according to a proteolytic cleavage pattern of at least one proteolytic agent.

9. The computer readable storage media of claim 8, wherein said at least one proteolytic agent is selected from the group consisting of a proteolytic enzyme and a proteolytic chemical.

10. The computer readable storage media of claim 9, wherein said proteolytic enzyme is selected from the group consisting of trypsin, chymotrypsin, subtilisin, pepsin, V8 protease, thrombin and elastase.

11. The computer readable storage media of claim 9, wherein said proteolytic chemical is selected from the group consisting of cyanogen bromide and 2-nitro-5-thiocyanobenzoate.

12. The computer readable storage media of claim 7, wherein said at least one parameter defining said characteristic of said amino acid sequence is selected from the group consisting of molecular weight, amino acid composition, hydrophobicity, hydrophilicity, charge, secondary structure, heterogeneity, length, post-translational modifications, polarity, solubility, amphipathic nature, sequence and immunogenicity.

13. A system for generating a database of amino acid sequences of at least one polypeptide of interest, the system comprising a processing unit, said processing unit executing a software application configured for:

(a) generating a plurality of proteolytic cleavage products from the at least one polypeptide of interest; and

(b) analyzing said plurality of proteolytic cleavage products according to at least one parameter defining a characteristic of an amino acid sequence.

14. The system of claim 13, wherein said plurality of proteolytic cleavage products are generated according to a proteolytic cleavage pattern of at least one proteolytic agent.

15. The system of claim 14, wherein said at least one proteolytic agent is selected from the group consisting of a proteolytic enzyme and a proteolytic chemical.

16. The system of claim 15, wherein said proteolytic enzyme is selected from the group consisting of trypsin, chymotrypsin, subtilisin, pepsin, V8 protease, thrombin and elastase.

17. The system of claim 15, wherein said proteolytic chemical is selected from the group consisting of cyanogen bromide and 2-nitro-5-thiocyanobenzoate.

18. The system of claim 13, wherein said at least one parameter defining said characteristic of said amino acid sequence is selected from the group consisting of molecular weight, amino acid composition, hydrophobicity, hydrophilicity, charge, secondary structure, heterogeneity, length, post-translational modifications, polarity, solubility, amphipathic nature, sequence and immunogenicity.

19. A kit for quantifying at least one polypeptide of interest, the kit comprising a plurality of peptides being generated according to information derived from computational analysis of the at least one polypeptide of interest, said computational analysis including generating a plurality of proteolytic cleavage products from the at least one polypeptide of interest.

20. The kit of claim 19, wherein said computational analysis further includes analysis of said plurality of proteolytic cleavage products according to

at least one parameter defining a characteristic of an amino acid sequence and selection of a set of proteolytic cleavage products from said plurality of proteolytic cleavage products according to predetermined criteria for each of said at least at least parameter.

21. The kit of claim 19, wherein said plurality of proteolytic cleavage products are generated according to information derived from a proteolytic cleavage pattern of at least one proteolytic agent.

22. The kit of claim 21, wherein said at least one proteolytic agent is selected from the group consisting of a proteolytic enzyme and a proteolytic chemical.

23. The kit of claim 22, wherein said proteolytic enzyme is selected from the group consisting of trypsin, chymotrypsin, subtilisin, pepsin, V8 protease, thrombin and elastase.

24. The kit of claim 22, wherein said proteolytic chemical is selected from the group consisting of cyanogen bromide and 2-nitro-5-thiocyanobenzoate.

25. The kit of claim 20, wherein said at least one parameter defining said characteristic of said amino acid sequence is selected from the group consisting of molecular weight, amino acid composition, hydrophobicity, hydrophilicity, charge, secondary structure, heterogeneity, length, post-translational modifications, polarity, solubility, amphipathic nature, sequence and immunogenicity.

26. The kit of claim 19, wherein said plurality of peptides are labeled.

27. The kit of claim 19, wherein said plurality of peptides are attached to a solid substrate.

28. The kit of claim 19, wherein each of said plurality of peptides is contained in an individual container.

29. The kit of claim 19, wherein said plurality of peptides are mixed in a single container.

30. The kit of claim 19, wherein said plurality of peptides are generated via peptide synthesis or proteolytic cleavage of the at least one polypeptide of interest.

31. A kit for quantifying at least one polypeptide of interest, the kit comprising a plurality of antibodies each capable of specifically recognizing at least one peptide of a plurality of peptides, said plurality of peptides being generated according to information derived from computational analysis of the at least one polypeptide of interest, said computational analysis including generating a plurality of proteolytic cleavage products from the at least one polypeptide of interest.

32. The kit of claim 31, wherein said computational analysis further includes analysis of said plurality of proteolytic cleavage products according to at least one parameter defining a characteristic of an amino acid sequence and selection of a set of proteolytic cleavage products from said plurality of

proteolytic cleavage products according to predetermined criteria for each of said at least at least parameter.

33. The kit of claim 31, wherein said plurality of proteolytic cleavage products are generated according to information derived from a proteolytic cleavage pattern of at least one proteolytic agent.

34. The kit of claim 33, wherein said at least one proteolytic agent is selected from the group consisting of a proteolytic enzyme and a proteolytic chemical.

35. The kit of claim 34, wherein said proteolytic enzyme is selected from the group consisting of trypsin, chymotrypsin, subtilisin, pepsin, V8 protease, thrombin and elastase.

36. The kit of claim 34, wherein said proteolytic chemical is selected from the group consisting of cyanogen bromide and 2-nitro-5-thiocyanobenzoate.

37. The kit of claim 32, wherein said at least one parameter defining said characteristic of said amino acid sequence is selected from the group consisting of molecular weight, amino acid composition, hydrophobicity, hydrophilicity, charge, secondary structure, heterogeneity, length, post-translational modifications, polarity, solubility, amphipathic nature, sequence and immunogenicity.

38. The kit of claim 31, wherein said plurality of antibodies are labeled.

39. The kit of claim 31, wherein said plurality of antibodies are attached to a solid substrate.

40. The kit of claim 31, wherein each of said plurality of antibodies is contained in an individual container.

41. The kit of claim 31, wherein said plurality of antibodies are mixed in a single container.

42. The kit of claim 31, wherein said plurality of peptides are generated via peptide synthesis or proteolytic cleavage of the at least one polypeptide of interest.

43. A method of quantifying at least one polypeptide of interest in a biological sample, the method comprising:

(a) contacting the biological sample with at least one proteolytic agent, so as to obtain a proteolysed biological sample;

(b) contacting said proteolysed biological sample with at least one antibody and at least one peptide of a plurality of peptides, wherein said antibody is capable of specifically binding said at least one peptide of said plurality of peptides, and further wherein said plurality of peptides are generated according to information derived from computational analysis of the at least one polypeptide of interest, said computational analysis including generating a plurality of proteolytic cleavage products from the at least one polypeptide of interest; and

(c) detecting presence, absence and/or level of antibody binding to thereby quantify the at least one polypeptide of interest in the biological sample.

44. The method of claim 43, wherein said at least one antibody is attached to a solid substrate.

45. The method of claim 44, wherein said solid substrate is configured as a microarray and said at least one antibody includes a plurality of antibodies each attached to said microarray in a regio-specific manner.

46. The method of claim 43, wherein said at least one antibody and/or said at least one peptide is labeled and whereas step (c) is effected by quantifying said label.

47. The method of claim 43, wherein said plurality of peptides are generated by peptide synthesis or proteolytic cleavage of the at least one polypeptide of interest.

48. The method of claim 43, wherein said computational analysis further includes analysis of said plurality of proteolytic cleavage products according to at least one parameter defining a characteristic of an amino acid sequence and selection of a set of proteolytic cleavage products from said plurality of proteolytic cleavage products according to predetermined criteria for each of said at least at least parameter.

49. The method of claim 43, wherein said plurality of proteolytic cleavage products are generated according to information derived from a proteolytic cleavage pattern of at least one proteolytic agent.

50. The method of claim 49, wherein said at least one proteolytic agent is selected from the group consisting of a proteolytic enzyme and a proteolytic chemical.

51. The method of claim 40, wherein said proteolytic enzyme is selected from the group consisting of trypsin, chymotrypsin, subtilisin, pepsin, V8 protease, thrombin and elastase.

52. The method of claim 50, wherein said proteolytic chemical is selected from the group consisting of cyanogen bromide and 2-nitro-5-thiocyanobenzoate.

53. The method of claim 48, wherein said at least one parameter defining said characteristic of said amino acid sequence is selected from the group consisting of molecular weight, amino acid composition, hydrophobicity, hydrophilicity, charge, secondary structure, heterogeneity, length, post-translational modifications, polarity, solubility, amphipathic nature, sequence and immunogenicity.

54. The method of claim 43, wherein said at least one peptide is attached to a solid substrate.

55. The method of claim 54, wherein said solid substrate is configured as a microarray and each of said plurality of peptides is attached to said microarray in a regio-specific manner.

56. A method of generating at least one antibody specific to a polypeptide of interest, the method comprising using at least one peptide to generate the at least one antibody specific to the polypeptide of interest, wherein said at least one peptide is generated according to information derived from computational analysis of the polypeptide of interest, said computational analysis including generating a plurality of proteolytic cleavage products from the polypeptide of interest.

57. The method of claim 56, wherein said computational analysis further includes analysis of said plurality of proteolytic cleavage products according to at least one parameter defining a characteristic of an amino acid sequence and selection of a set of proteolytic cleavage products from said plurality of proteolytic cleavage products according to predetermined criteria for each of said at least at least parameter.

58. The method of claim 56, wherein said plurality of proteolytic cleavage products are generated according to information derived from a proteolytic cleavage pattern of at least one proteolytic agent.

59. The method of claim 58, wherein said at least one proteolytic agent is selected from the group consisting of a proteolytic enzyme and a proteolytic chemical.

60. The method of claim 59, wherein said proteolytic enzyme is selected from the group consisting of trypsin, chymotrypsin, subtilisin, pepsin, V8 protease, thrombin and elastase.

61. The method of claim 59, wherein said proteolytic chemical is selected from the group consisting of cyanogen bromide and 2-nitro-5-thiocyanobenzoate.

62. The method of claim 57, wherein said at least one parameter defining said characteristic of said amino acid sequence is selected from the group consisting of molecular weight, amino acid composition, hydrophobicity, hydrophilicity, charge, secondary structure, heterogeneity, length, post-translational modifications, polarity, solubility, amphipathic nature, sequence and immunogenicity.

63. The method of claim 56, wherein said at least one peptide is generated by peptide synthesis or proteolytic cleavage of the at least one polypeptide of interest.